

8/22/06

ZM

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	24	thomas.in. and gardella.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:51
L2	22	henry.in. and kronenberg.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:51
L3	163	potts.in. and john.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:52
L4	183	l1 or l2 or l3	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:52
L5	35	l4 and parathyroid	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:53
L6	23	L5 and (truncat\$4)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:53
L7	6	L5 and ((truncat\$4) same extracellular)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:56
L8	1	l4 and hdelnt\$4	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:56
L10	3	l4 and (hdelnt\$4 or delnt\$4 or hdel-nt\$4 or h-delnt\$4 or h-del-nt\$4)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:57

## EAST Search History

L11	0	I4 and E1-G\$4	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:57
L12	0	I4 and E1G\$4	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:58
L13	0	I4 and delta-nt\$4	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:58
L14	0	I4 and r-delta-nt\$4	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:58
L17	32	(gardella.in. or kronenberg.in. or potts.in.) and (parathyroid)	FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:10
L18	21	(gardella.in. or kronenberg.in. or potts.in.) and (parathyroid) and receptor	FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:11
L19	0	(r-delta-e1\$4 or rdelta-e1\$4 or rdeltae1\$4)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:12
L20	1	26-181	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:12
L21	287	(residue near5 "26") and (residue near5 "181")	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:13
L22	35	(residue near5 "26") same (residue near5 "181")	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:13

## EAST Search History

L23	16	(residue near5 "26") same (residue near5 "181") and parathyroid	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:17
L24	14	(residue near5 "26") same (residue near5 "181") and (parathyroid same receptor)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:17
L25	1	(r-delta-nt\$4 or rdeltant\$4 or rdelta-nt\$4) or (r adj delta adj nt\$4)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:22
L26	84	(pth.ti. or parathyroid.ti.) and receptor.ti.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:21
L27	282	(parathyroid adj hormone adj receptor) or (pth adj receptor) same (agonist or antagonist)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23
L28	110	((parathyroid adj hormone adj receptor) or (pth adj receptor)) same (agonist or antagonist)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23
L29	11	"20030144209".pn. or "20030162256".pn. or "20030166838".pn. or "6803213".pn. or "20050026839".pn. or "4086196".pn. or "5217896".pn. or "6417333".pn. or "6495662".pn. or "6537965".pn. or "6541220".pn.	US-PGPUB; USPAT	OR	ON	2006/08/22 12:23
L30	449	(parathyroid adj hormone adj receptor) or (pth adj receptor)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23
L31	82	((parathyroid adj hormone adj receptor) or (pth adj receptor) with (agonist or antagonist)) same (method or assay or screen\$3)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23

## EAST Search History

L32	275	(parathyroid adj hormone adj receptor) or (pth adj receptor) with (agonist or antagonist)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23
L33	6	"6537965".pn. or "5494806".pn. or "200040698".pn.	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23
L34	10	pth.ti. and receptor.ti.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23
L35	80	parathyroid.ti. and receptor.ti.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23
L36	1484	(parathyroid near15 receptor) or (pthr-1 or pthr1 or hpthr-1 or hpthr1 or pthr or hpthr) or ((pth1 or pth-1 or hpth1 or hpth-1) near5 receptor)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:25
L37	76	L36 and (extracellular near30 (trunc\$7 or delet\$7))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:26
L38	65	L36 and receptor and (extracellular near15 (trunc\$7 or delet\$7))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:26
L39	49	L36 and receptor and (extracellular near5 (trunc\$7 or delet\$7))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:26

8/22/06  
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# STN SEARCH HISTORY

=> d his

(FILE 'HOME' ENTERED AT 10:55:59 ON 22 AUG 2006)

FILE 'MEDLINE, EMBASE, BIOSIS, SCISEARCH, DISSABS, TOXCENTER' ENTERED AT 10:56:40 ON 22 AUG 2006

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L1      708 S (GARDELLA T?/AU) OR (GARDELLA J?/AU)
L2      3076 S (KRONENBERG H?/AU) OR (KRONENBERG M?/AU)
L3      2810 S (POTTS J?/AU) OR (POTTS T?/AU)
L4      6279 S L1 OR L2 OR L3
L5      1448 S L4 AND PARATHYROID
L6      441 S L4 AND (PARATHYROID (5A) RECEPTOR)
L7      304 S (PTHR-1 OR PTHR1 OR HPTHR-1 OR HPTHR1)
L8      390 S ((PTH1 OR PTH-1) (2A) RECEPTOR)
L9      525 S (PTHR)
L10     9 S PTHR-DELNT
L11     5 S R-DELTA-NT
L12     1 S RDELTA-NT
L13     0 S R-DELTA-E1-G
L14     0 S R-DELTA-E1G
L15     0 S R-DELTA-E1G
L16     0 S RDELTA-E1G
L17     0 S RDELTA-E1-G
L18     0 S RDELTA-E1-G
L19     21 S 26-181
L20     1221 S L7 OR L8 OR L9 OR L10 OR L11 OR L12 OR L19
L21     119 S L20 AND L4
L22     37 DUP REM L21 (82 DUPLICATES REMOVED)
L23     13 DUP REM L19 (8 DUPLICATES REMOVED)
L24     15 S L10 OR L11 OR L12
L25     4 DUP REM L24 (11 DUPLICATES REMOVED)
L26     8469 S (PARATHYROID) (15A) (RECEPTOR)
L27     77 S L26 AND (EXTRACELLULAR) AND (TRUNC?)
L28     26 DUP REM L27 (51 DUPLICATES REMOVED)
L29     1 S L26 AND ((EXTRACELLULAR) (5A) (TRUNC?))
L30     1200 S L7 OR L8 OR L9
L31     1 S L30 AND (EXTRACELLULAR (5A) (TRUNC? OR DELET?))
```

=> log y

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2006, 17:02:23 ; Search time 266.154 Seconds  
(without alignments)  
9279.834 Million cell updates/sec

Title: US-09-869-565-1  
Perfect score: 1320  
Sequence: 1 atgggggcccggatcgc.....tcatgtgactgggcactagg 1320

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1243.2	94.2	2051	2	US-07-864-475A-3	Sequence 3, Appli
2	1243.2	94.2	2051	2	US-08-468-249A-3	Sequence 3, Appli
3	966.8	73.2	1948	3	US-09-016-434-1253	Sequence 1253, Ap
4	965.2	73.1	2010	2	US-07-864-475A-4	Sequence 4, Appli
5	965.2	73.1	2010	2	US-08-468-249A-4	Sequence 4, Appli
6	959.6	72.7	1782	3	US-09-826-509-562	Sequence 562, App
7	691.6	52.4	1863	2	US-07-864-475A-2	Sequence 2, Appli
8	691.6	52.4	1863	2	US-08-468-249A-2	Sequence 2, Appli
9	681.2	51.6	1862	2	US-07-864-475A-1	Sequence 1, Appli
10	681.2	51.6	1862	2	US-08-468-249A-1	Sequence 1, Appli
11	554.6	42.0	1609	3	US-09-449-632-1	Sequence 1, Appli
12	387.4	29.3	2003	3	US-08-468-011A-1	Sequence 1, Appli
13	387.4	29.3	2003	3	US-09-236-468A-1	Sequence 1, Appli
14	387.4	29.3	2003	7	PCT-US95-07085-1	Sequence 1, Appli
15	387.4	29.3	2152	3	US-09-449-632-3	Sequence 3, Appli
16	387.4	29.3	2641	3	US-09-016-434-1463	Sequence 1463, Ap
17	385.8	29.2	1653	3	US-09-826-509-564	Sequence 564, App
18	196.6	14.9	1377	2	US-08-112-817C-1	Sequence 1, Appli
19	192.4	14.6	1374	3	US-09-826-509-578	Sequence 578, App
20	177.8	13.5	2025	3	US-09-016-434-1063	Sequence 1063, Ap
21	176.2	13.3	1401	3	US-09-826-509-506	Sequence 506, App
22	175.4	13.3	1578	3	US-09-016-434-1377	Sequence 1377, Ap
23	175.4	13.3	1809	2	US-08-453-956-24	Sequence 24, Appl
24	175.4	13.3	1809	2	US-08-086-631-24	Sequence 24, Appl
25	175.4	13.3	1809	2	US-08-452-930-24	Sequence 24, Appl
26	175.4	13.3	1809	7	PCT-US93-08174-24	Sequence 24, Appl
27	175.4	13.3	2034	3	US-10-010-065-5	Sequence 5, Appli
28	172.8	13.1	1323	3	US-09-826-509-566	Sequence 566, App
29	172.8	13.1	1616	3	US-09-016-434-1451	Sequence 1451, Ap
30	169.4	12.8	2616	3	US-09-016-434-1358	Sequence 1358, Ap
31	168.4	12.8	1944	3	US-10-010-065-1	Sequence 1, Appli
32	168.4	12.8	3066	2	US-08-142-439A-1	Sequence 1, Appli
33	168.4	12.8	3066	2	US-08-869-477-1	Sequence 1, Appli
34	166.2	12.6	1455	2	US-08-811-897A-31	Sequence 31, Appl
35	166.2	12.6	1455	2	US-08-855-213-31	Sequence 31, Appl
36	166.2	12.6	1455	3	US-09-201-474-31	Sequence 31, Appl
37	166.2	12.6	2730	2	US-08-811-897A-39	Sequence 39, Appl
38	166.2	12.6	2730	2	US-08-855-213-39	Sequence 39, Appl
39	166.2	12.6	2730	3	US-09-201-474-39	Sequence 39, Appl
40	158.8	12.0	1875	2	US-08-453-956-14	Sequence 14, Appl
41	158.8	12.0	1875	2	US-08-086-631-14	Sequence 14, Appl
42	158.8	12.0	1875	2	US-08-452-930-14	Sequence 14, Appl

43	158.8	12.0	1875	7	PCT-US93-08174-14	Sequence 14, Appl
44	151.4	11.5	1401	2	US-08-811-897A-32	Sequence 32, Appl
45	151.4	11.5	1401	2	US-08-855-213-32	Sequence 32, Appl

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2006, 17:12:01 ; Search time 1863.59 Seconds  
 (without alignments)  
 8703.460 Million cell updates/sec

Title: US-09-869-565-1  
 Perfect score: 1320  
 Sequence: 1 atgggggcccggatcgc.....tcatgtgactgggcactagg 1320

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published\_Applications\_NA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
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- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
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- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1243.2	94.2	2051	7 US-10-267-730-3	Sequence 3, Appli
2	1241.6	94.1	2065	8 US-10-152-319A-1741	Sequence 1741, Ap
3	1241.6	94.1	2065	16 US-11-036-196-1741	Sequence 1741, Ap
4	1236.4	93.7	2065	16 US-11-136-527-2547	Sequence 2547, Ap
5	1229.6	93.2	1776	3 US-09-943-446-3	Sequence 3, Appli
6	1146.4	86.8	1776	3 US-09-943-446-4	Sequence 4, Appli
7	1146.4	86.8	1776	3 US-09-943-446-5	Sequence 5, Appli
8	966.8	73.2	1948	6 US-10-225-567A-228	Sequence 228, App
9	966.8	73.2	1948	7 US-10-305-720-1253	Sequence 1253, Ap
10	966.8	73.2	1948	10 US-10-956-157-395	Sequence 395, App
11	966.8	73.2	2282	9 US-10-723-860-5567	Sequence 5567, Ap
12	965.2	73.1	2010	7 US-10-267-730-4	Sequence 4, Appli
13	965.2	73.1	2171	9 US-10-723-860-1005	Sequence 1005, Ap
14	959.6	72.7	1782	3 US-09-826-509-562	Sequence 562, App
15	959.6	72.7	1782	9 US-10-925-095-562	Sequence 562, App
16	958.2	72.6	1779	10 US-10-505-486-14	Sequence 14, Appl
17	902.2	68.3	2177	3 US-09-943-446-1	Sequence 1, Appli
18	899	68.1	1788	3 US-09-943-446-2	Sequence 2, Appli
19	758.4	57.5	2192	7 US-10-062-674-1564	Sequence 1564, Ap
20	691.6	52.4	1863	7 US-10-267-730-2	Sequence 2, Appli
21	681.2	51.6	1862	7 US-10-267-730-1	Sequence 1, Appli
22	610.8	46.3	681	8 US-10-332-859-229	Sequence 229, App
23	554.6	42.0	1609	7 US-10-372-095-1	Sequence 1, Appli
24	462.4	35.0	637	8 US-10-332-859-9	Sequence 9, Appli
25	393	29.8	600	16 US-11-136-527-6643	Sequence 6643, Ap
26	387.4	29.3	1896	7 US-10-295-027-523	Sequence 523, App
27	387.4	29.3	2003	3 US-09-996-569-1	Sequence 1, Appli
28	387.4	29.3	2003	9 US-10-921-218-1	Sequence 1, Appli
29	387.4	29.3	2152	7 US-10-372-095-3	Sequence 3, Appli
30	387.4	29.3	2641	6 US-10-225-567A-226	Sequence 226, App
31	387.4	29.3	2641	7 US-10-295-027-525	Sequence 525, App
32	387.4	29.3	2641	7 US-10-295-027-850	Sequence 850, App
33	387.4	29.3	2641	7 US-10-305-720-1463	Sequence 1463, Ap
34	387.4	29.3	2641	8 US-10-283-975A-70	Sequence 70, Appl
35	387.4	29.3	2641	9 US-10-723-860-2138	Sequence 2138, Ap
36	387.4	29.3	3071	9 US-10-723-860-6394	Sequence 6394, Ap



37	385.8	29.2	1653	3	US-09-826-509-564	Sequence 564, App
38	385.8	29.2	1653	9	US-10-925-095-564	Sequence 564, App
39	359	27.2	1977	16	US-11-136-527-2881	Sequence 2881, Ap
40	331.6	25.1	600	10	US-10-956-157-5630	Sequence 5630, Ap
41	331.6	25.1	600	13	US-11-060-756-1955	Sequence 1955, Ap
42	331.6	25.1	600	13	US-11-060-756-6227	Sequence 6227, Ap
43	328.6	24.9	343	7	US-10-062-674-392	Sequence 392, App
44	265	20.1	21704	7	US-10-017-161-709	Sequence 709, App
45	265	20.1	21704	7	US-10-292-798-621	Sequence 621, App

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2006, 17:13:58 ; Search time 212.308 Seconds  
 (without alignments)  
 9503.772 Million cell updates/sec

Title: US-09-869-565-1  
 Perfect score: 1320  
 Sequence: 1 atgggggcccgcggatcgc.....tcatgtgactgggcactagg 1320

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 2187952 seqs, 764289321 residues

Total number of hits satisfying chosen parameters: 4375904

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published\_Applications\_NA\_New:\*  
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 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	965.2	73.1	2171	8	US-11-266-748A-31864	Sequence 31864, A
2	653.8	49.5	1037	8	US-11-266-748A-72888	Sequence 72888, A
3	653.8	49.5	1037	8	US-11-266-748A-107536	Sequence 107536, A
c 4	653.8	49.5	1037	8	US-11-266-748A-125699	Sequence 125699, A
5	637.6	48.3	1000	8	US-11-266-748A-115117	Sequence 115117, A
c 6	637.6	48.3	1000	8	US-11-266-748A-157281	Sequence 157281, A
7	637.6	48.3	1000	8	US-11-266-748A-220526	Sequence 220526, A
8	637.6	48.3	1000	8	US-11-266-748A-283699	Sequence 283699, A
c 9	637.6	48.3	1000	8	US-11-266-748A-335128	Sequence 335128, A
10	637.6	48.3	1000	8	US-11-266-748A-393467	Sequence 393467, A
c 11	637.6	48.3	1000	8	US-11-266-748A-464513	Sequence 464513, A
12	326.2	24.7	651	8	US-11-266-748A-72887	Sequence 72887, A
13	326.2	24.7	651	8	US-11-266-748A-107535	Sequence 107535, A
c 14	326.2	24.7	651	8	US-11-266-748A-125698	Sequence 125698, A
c 15	315.6	23.9	718	6	US-10-473-173-255	Sequence 255, Appl
16	315	23.9	685	8	US-11-266-748A-365289	Sequence 365289, A
c 17	315	23.9	685	8	US-11-266-748A-448668	Sequence 448668, A
18	221.6	16.8	544	8	US-11-266-748A-264658	Sequence 264658, A
c 19	221.6	16.8	544	8	US-11-266-748A-325175	Sequence 325175, A
20	194	14.7	2771	8	US-11-266-748A-29527	Sequence 29527, A
21	177.8	13.5	2025	8	US-11-266-748A-31931	Sequence 31931, A
22	174.4	13.2	1323	8	US-11-266-748A-25118	Sequence 25118, A
23	168.4	12.8	1523	6	US-10-504-973-55	Sequence 55, Appl
24	158.6	12.0	1000	8	US-11-266-748A-115926	Sequence 115926, A
c 25	158.6	12.0	1000	8	US-11-266-748A-158090	Sequence 158090, A
26	158.6	12.0	1000	8	US-11-266-748A-396071	Sequence 396071, A
c 27	158.6	12.0	1000	8	US-11-266-748A-467117	Sequence 467117, A
28	147.6	11.2	1000	8	US-11-266-748A-284911	Sequence 284911, A
c 29	147.6	11.2	1000	8	US-11-266-748A-336340	Sequence 336340, A
30	147.6	11.2	1000	8	US-11-266-748A-395056	Sequence 395056, A
c 31	147.6	11.2	1000	8	US-11-266-748A-466102	Sequence 466102, A
32	138.2	10.5	1039	8	US-11-266-748A-352772	Sequence 352772, A
33	138.2	10.5	1039	8	US-11-266-748A-384234	Sequence 384234, A
c 34	138.2	10.5	1039	8	US-11-266-748A-436151	Sequence 436151, A
c 35	132.6	10.0	986	8	US-11-266-748A-2319	Sequence 2319, Ap
36	132.6	10.0	986	8	US-11-266-748A-62948	Sequence 62948, A
c 37	132.6	10.0	986	8	US-11-266-748A-65780	Sequence 65780, A
38	128.4	9.7	1000	8	US-11-266-748A-393752	Sequence 393752, A
c 39	128.4	9.7	1000	8	US-11-266-748A-464798	Sequence 464798, A
40	127.4	9.7	1817	8	US-11-266-748A-59257	Sequence 59257, A
41	127.4	9.7	3958	8	US-11-266-748A-57216	Sequence 57216, A
42	120.8	9.2	1154	8	US-11-266-748A-367011	Sequence 367011, A
43	120.8	9.2	1154	8	US-11-266-748A-388713	Sequence 388713, A

c	44	120.8	9.2	1154	8	US-11-266-748A-450390	Sequence 450390,
c	45	116.6	8.8	908	8	US-11-266-748A-366994	Sequence 366994,

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2006, 17:02:23 ; Search time 252.846 Seconds  
 (without alignments)  
 9279.834 Million cell updates/sec

Title: US-09-869-565-1\_COPY\_67\_1320  
 Perfect score: 1254  
 Sequence: 1 tatgcgctggagggtatttga.....tcatgtgactgggcactagg 1254

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
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 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1243.2	99.1	2051	2	US-07-864-475A-3	Sequence 3, Appli
2	1243.2	99.1	2051	2	US-08-468-249A-3	Sequence 3, Appli
3	966.8	77.1	1948	3	US-09-016-434-1253	Sequence 1253, Ap
4	965.2	77.0	2010	2	US-07-864-475A-4	Sequence 4, Appli
5	965.2	77.0	2010	2	US-08-468-249A-4	Sequence 4, Appli
6	959.6	76.5	1782	3	US-09-826-509-562	Sequence 562, App
7	691.6	55.2	1863	2	US-07-864-475A-2	Sequence 2, Appli
8	691.6	55.2	1863	2	US-08-468-249A-2	Sequence 2, Appli
9	681.2	54.3	1862	2	US-07-864-475A-1	Sequence 1, Appli
10	681.2	54.3	1862	2	US-08-468-249A-1	Sequence 1, Appli
11	554.6	44.2	1609	3	US-09-449-632-1	Sequence 1, Appli
12	387.4	30.9	2003	3	US-08-468-011A-1	Sequence 1, Appli
13	387.4	30.9	2003	3	US-09-236-468A-1	Sequence 1, Appli
14	387.4	30.9	2003	7	PCT-US95-07085-1	Sequence 1, Appli
15	387.4	30.9	2152	3	US-09-449-632-3	Sequence 3, Appli
16	387.4	30.9	2641	3	US-09-016-434-1463	Sequence 1463, Ap
17	385.8	30.8	1653	3	US-09-826-509-564	Sequence 564, App
18	196.6	15.7	1377	2	US-08-112-817C-1	Sequence 1, Appli
19	192.4	15.3	1374	3	US-09-826-509-578	Sequence 578, App
20	177.8	14.2	2025	3	US-09-016-434-1063	Sequence 1063, Ap
21	176.2	14.1	1401	3	US-09-826-509-506	Sequence 506, App
22	175.4	14.0	1578	3	US-09-016-434-1377	Sequence 1377, Ap
23	175.4	14.0	1809	2	US-08-453-956-24	Sequence 24, Appl
24	175.4	14.0	1809	2	US-08-086-631-24	Sequence 24, Appl
25	175.4	14.0	1809	2	US-08-452-930-24	Sequence 24, Appl
26	175.4	14.0	1809	7	PCT-US93-08174-24	Sequence 24, Appl
27	175.4	14.0	2034	3	US-10-010-065-5	Sequence 5, Appli
28	172.8	13.8	1323	3	US-09-826-509-566	Sequence 566, App
29	172.8	13.8	1616	3	US-09-016-434-1451	Sequence 1451, Ap
30	169.4	13.5	2616	3	US-09-016-434-1358	Sequence 1358, Ap
31	168.4	13.4	1944	3	US-10-010-065-1	Sequence 1, Appli
32	168.4	13.4	3066	2	US-08-142-439A-1	Sequence 1, Appli
33	168.4	13.4	3066	2	US-08-869-477-1	Sequence 1, Appli
34	166.2	13.3	1455	2	US-08-811-897A-31	Sequence 31, Appl
35	166.2	13.3	1455	2	US-08-855-213-31	Sequence 31, Appl
36	166.2	13.3	1455	3	US-09-201-474-31	Sequence 31, Appl
37	166.2	13.3	2730	2	US-08-811-897A-39	Sequence 39, Appl
38	166.2	13.3	2730	2	US-08-855-213-39	Sequence 39, Appl
39	166.2	13.3	2730	3	US-09-201-474-39	Sequence 39, Appl
40	158.8	12.7	1875	2	US-08-453-956-14	Sequence 14, Appl
41	158.8	12.7	1875	2	US-08-086-631-14	Sequence 14, Appl
42	158.8	12.7	1875	2	US-08-452-930-14	Sequence 14, Appl

43	158.8	12.7	1875	7	PCT-US93-08174-14	Sequence 14, Appl
44	151.4	12.1	1401	2	US-08-811-897A-32	Sequence 32, Appl
45	151.4	12.1	1401	2	US-08-855-213-32	Sequence 32, Appl

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2006, 17:12:01 ; Search time 1770.41 Seconds  
 (without alignments)  
 8703.460 Million cell updates/sec

Title: US-09-869-565-1\_COPY\_67\_1320  
 Perfect score: 1254  
 Sequence: 1 tatgcgctggagggtatttga.....tcatgtgactgggcactagg 1254

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published\_Applications\_NA\_Main:\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
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- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1243.2	99.1	2051	7	US-10-267-730-3	Sequence 3, Appli
2	1241.6	99.0	2065	8	US-10-152-319A-1741	Sequence 1741, Ap
3	1241.6	99.0	2065	16	US-11-036-196-1741	Sequence 1741, Ap
4	1236.4	98.6	2065	16	US-11-136-527-2547	Sequence 2547, Ap
5	1229.6	98.1	1776	3	US-09-943-446-3	Sequence 3, Appli
6	1146.4	91.4	1776	3	US-09-943-446-4	Sequence 4, Appli
7	1146.4	91.4	1776	3	US-09-943-446-5	Sequence 5, Appli
8	966.8	77.1	1948	6	US-10-225-567A-228	Sequence 228, App
9	966.8	77.1	1948	7	US-10-305-720-1253	Sequence 1253, Ap
10	966.8	77.1	1948	10	US-10-956-157-395	Sequence 395, App
11	966.8	77.1	2282	9	US-10-723-860-5567	Sequence 5567, Ap
12	965.2	77.0	2010	7	US-10-267-730-4	Sequence 4, Appli
13	965.2	77.0	2171	9	US-10-723-860-1005	Sequence 1005, Ap
14	959.6	76.5	1782	3	US-09-826-509-562	Sequence 562, App
15	959.6	76.5	1782	9	US-10-925-095-562	Sequence 562, App
16	958.2	76.4	1779	10	US-10-505-486-14	Sequence 14, Appl
17	902.2	71.9	2177	3	US-09-943-446-1	Sequence 1, Appli
18	899	71.7	1788	3	US-09-943-446-2	Sequence 2, Appli
19	758.4	60.5	2192	7	US-10-062-674-1564	Sequence 1564, Ap
20	691.6	55.2	1863	7	US-10-267-730-2	Sequence 2, Appli
21	681.2	54.3	1862	7	US-10-267-730-1	Sequence 1, Appli
22	610.8	48.7	681	8	US-10-332-859-229	Sequence 229, App
23	554.6	44.2	1609	7	US-10-372-095-1	Sequence 1, Appli
24	462.4	36.9	637	8	US-10-332-859-9	Sequence 9, Appli
25	393	31.3	600	16	US-11-136-527-6643	Sequence 6643, Ap
26	387.4	30.9	1896	7	US-10-295-027-523	Sequence 523, App
27	387.4	30.9	2003	3	US-09-996-569-1	Sequence 1, Appli
28	387.4	30.9	2003	9	US-10-921-218-1	Sequence 1, Appli
29	387.4	30.9	2152	7	US-10-372-095-3	Sequence 3, Appli
30	387.4	30.9	2641	6	US-10-225-567A-226	Sequence 226, App
31	387.4	30.9	2641	7	US-10-295-027-525	Sequence 525, App
32	387.4	30.9	2641	7	US-10-295-027-850	Sequence 850, App
33	387.4	30.9	2641	7	US-10-305-720-1463	Sequence 1463, Ap
34	387.4	30.9	2641	8	US-10-283-975A-70	Sequence 70, Appl
35	387.4	30.9	2641	9	US-10-723-860-2138	Sequence 2138, Ap
36	387.4	30.9	3071	9	US-10-723-860-6394	Sequence 6394, Ap

37	385.8	30.8	1653	3	US-09-826-509-564	Sequence 564, App
38	385.8	30.8	1653	9	US-10-925-095-564	Sequence 564, App
39	359	28.6	1977	16	US-11-136-527-2881	Sequence 2881, Ap
40	331.6	26.4	600	10	US-10-956-157-5630	Sequence 5630, Ap
41	331.6	26.4	600	13	US-11-060-756-1955	Sequence 1955, Ap
42	331.6	26.4	600	13	US-11-060-756-6227	Sequence 6227, Ap
43	328.6	26.2	343	7	US-10-062-674-392	Sequence 392, App
44	265	21.1	21704	7	US-10-017-161-709	Sequence 709, App
45	265	21.1	21704	7	US-10-292-798-621	Sequence 621, App

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2006, 17:13:58 ; Search time 201.692 Seconds  
 (without alignments)  
 9503.772 Million cell updates/sec

Title: US-09-869-565-1\_COPY\_67\_1320  
 Perfect score: 1254  
 Sequence: 1 tatgcgctggagggtatttga.....tcattgtgactgggcactagg 1254

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 2187952 seqs, 764289321 residues

Total number of hits satisfying chosen parameters: 4375904

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published\_Applications\_NA\_New:\*  
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 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	965.2	77.0	2171	8	US-11-266-748A-31864	Sequence 31864, A
2	653.8	52.1	1037	8	US-11-266-748A-72888	Sequence 72888, A
3	653.8	52.1	1037	8	US-11-266-748A-107536	Sequence 107536,
c 4	653.8	52.1	1037	8	US-11-266-748A-125699	Sequence 125699,
5	637.6	50.8	1000	8	US-11-266-748A-115117	Sequence 115117,
c 6	637.6	50.8	1000	8	US-11-266-748A-157281	Sequence 157281,
7	637.6	50.8	1000	8	US-11-266-748A-220526	Sequence 220526,
8	637.6	50.8	1000	8	US-11-266-748A-283699	Sequence 283699,
c 9	637.6	50.8	1000	8	US-11-266-748A-335128	Sequence 335128,
10	637.6	50.8	1000	8	US-11-266-748A-393467	Sequence 393467,
c 11	637.6	50.8	1000	8	US-11-266-748A-464513	Sequence 464513,
12	326.2	26.0	651	8	US-11-266-748A-72887	Sequence 72887, A
13	326.2	26.0	651	8	US-11-266-748A-107535	Sequence 107535,
c 14	326.2	26.0	651	8	US-11-266-748A-125698	Sequence 125698,
c 15	315.6	25.2	718	6	US-10-473-173-255	Sequence 255, App
16	315	25.1	685	8	US-11-266-748A-365289	Sequence 365289,
c 17	315	25.1	685	8	US-11-266-748A-448668	Sequence 448668,
18	221.6	17.7	544	8	US-11-266-748A-264658	Sequence 264658,
c 19	221.6	17.7	544	8	US-11-266-748A-325175	Sequence 325175,
20	194	15.5	2771	8	US-11-266-748A-29527	Sequence 29527, A
21	177.8	14.2	2025	8	US-11-266-748A-31931	Sequence 31931, A
22	174.4	13.9	1323	8	US-11-266-748A-25118	Sequence 25118, A
23	168.4	13.4	1523	6	US-10-504-973-55	Sequence 55, Appl
24	158.6	12.6	1000	8	US-11-266-748A-115926	Sequence 115926,
c 25	158.6	12.6	1000	8	US-11-266-748A-158090	Sequence 158090,
26	158.6	12.6	1000	8	US-11-266-748A-396071	Sequence 396071,
c 27	158.6	12.6	1000	8	US-11-266-748A-467117	Sequence 467117,
28	147.6	11.8	1000	8	US-11-266-748A-284911	Sequence 284911,
c 29	147.6	11.8	1000	8	US-11-266-748A-336340	Sequence 336340,
30	147.6	11.8	1000	8	US-11-266-748A-395056	Sequence 395056,
c 31	147.6	11.8	1000	8	US-11-266-748A-466102	Sequence 466102,
32	138.2	11.0	1039	8	US-11-266-748A-352772	Sequence 352772,
33	138.2	11.0	1039	8	US-11-266-748A-384234	Sequence 384234,
c 34	138.2	11.0	1039	8	US-11-266-748A-436151	Sequence 436151,
c 35	132.6	10.6	986	8	US-11-266-748A-2319	Sequence 2319, Ap
36	132.6	10.6	986	8	US-11-266-748A-62948	Sequence 62948, A
c 37	132.6	10.6	986	8	US-11-266-748A-65780	Sequence 65780, A
38	128.4	10.2	1000	8	US-11-266-748A-393752	Sequence 393752,
c 39	128.4	10.2	1000	8	US-11-266-748A-464798	Sequence 464798,
40	127.4	10.2	1817	8	US-11-266-748A-59257	Sequence 59257, A
41	127.4	10.2	3958	8	US-11-266-748A-57216	Sequence 57216, A
42	120.8	9.6	1154	8	US-11-266-748A-367011	Sequence 367011,
43	120.8	9.6	1154	8	US-11-266-748A-388713	Sequence 388713,



c	44	120.8	9.6	1154	8	US-11-266-748A-450390	Sequence 450390,
c	45	116.6	9.3	908	8	US-11-266-748A-366994	Sequence 366994,

3M  
8/22/06

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OM protein - protein search, using sw model

Run on: July 26, 2006, 21:23:07 ; Search time 37.4469 Seconds  
(without alignments)  
1016.794 Million cell updates/sec

Title: US-09-869-565-2  
Perfect score: 2283  
Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGSARPPPLLQEGWETVM 435

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2195	96.1	591	1	US-08-468-249A-20	Sequence 20, Appl
2	2008	88.0	593	2	US-09-631-603-21	Sequence 21, Appl
3	2002	87.7	593	1	US-08-468-249A-21	Sequence 21, Appl
4	2002	87.7	593	2	US-09-826-509-563	Sequence 563, App
5	1710	74.9	585	1	US-08-142-439A-6	Sequence 6, Appli
6	1710	74.9	585	1	US-08-142-551B-125	Sequence 125, App
7	1710	74.9	585	1	US-08-869-477-6	Sequence 6, Appli
8	1710	74.9	585	1	US-08-468-249A-19	Sequence 19, Appl
9	1551	67.9	515	1	US-08-468-249A-18	Sequence 18, Appl
10	1465	64.2	536	2	US-09-449-632-2	Sequence 2, Appli
11	1130	49.5	542	2	US-09-449-632-4	Sequence 4, Appli
12	1068	46.8	575	2	US-09-449-632-5	Sequence 5, Appli
13	1050.5	46.0	550	2	US-09-631-603-20	Sequence 20, Appl
14	1044.5	45.8	550	2	US-09-826-509-565	Sequence 565, App
15	1036	45.4	541	2	US-08-468-011A-2	Sequence 2, Appli
16	1036	45.4	541	2	US-09-236-468A-2	Sequence 2, Appli
17	1036	45.4	541	5	PCT-US95-07085-2	Sequence 2, Appli
18	960.5	42.1	207	2	US-08-811-519-31	Sequence 31, Appl
19	776	34.0	459	2	US-09-694-519-4	Sequence 4, Appli
20	775.5	34.0	1324	1	US-08-811-897A-56	Sequence 56, Appl
21	775.5	34.0	1324	2	US-09-201-474-56	Sequence 56, Appl
22	773.5	33.9	444	2	US-09-694-519-6	Sequence 6, Appli
23	772	33.8	459	2	US-09-694-519-3	Sequence 3, Appli
24	772	33.8	459	2	US-09-694-519-8	Sequence 8, Appli
25	762.5	33.4	458	1	US-08-112-817C-2	Sequence 2, Appli
26	762.5	33.4	458	2	US-09-694-519-5	Sequence 5, Appli
27	762.5	33.4	458	2	US-09-694-519-7	Sequence 7, Appli
28	757.5	33.2	449	1	US-08-142-439A-5	Sequence 5, Appli
29	757.5	33.2	449	1	US-08-869-477-5	Sequence 5, Appli
30	752.5	33.0	457	2	US-09-631-603-23	Sequence 23, Appl
31	752.5	33.0	457	2	US-09-694-519-1	Sequence 1, Appli
32	747	32.7	440	2	US-09-631-603-22	Sequence 22, Appl
33	746.5	32.7	457	2	US-09-826-509-579	Sequence 579, App
34	741	32.5	460	2	US-09-694-519-2	Sequence 2, Appli
35	738	32.3	440	2	US-09-826-509-567	Sequence 567, App
36	718	31.4	447	2	US-09-694-519-9	Sequence 9, Appli
37	687	30.1	448	1	US-08-811-897A-22	Sequence 22, Appl
38	687	30.1	448	1	US-08-855-213-22	Sequence 22, Appl
39	687	30.1	448	2	US-09-201-474-22	Sequence 22, Appl
40	687	30.1	468	2	US-09-631-603-19	Sequence 19, Appl
41	687	30.1	525	1	US-08-811-897A-23	Sequence 23, Appl
42	687	30.1	525	1	US-08-855-213-23	Sequence 23, Appl
43	687	30.1	525	2	US-09-201-474-23	Sequence 23, Appl
44	684	30.0	448	1	US-08-811-897A-18	Sequence 18, Appl
45	684	30.0	448	1	US-08-855-213-18	Sequence 18, Appl

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: July 26, 2006, 21:39:27 ; Search time 132.86 Seconds  
(without alignments)  
1516.626 Million cell updates/sec

Title: US-09-869-565-2  
Perfect score: 2283  
Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGSARPPPLLQEGWETVM 435

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2195	96.1	591	4	US-10-267-730-20
2	2187	95.8	591	3	US-09-943-446-7
3	2146	94.0	591	3	US-09-943-446-8
4	2008	88.0	593	3	US-09-943-446-9
5	2008	88.0	593	4	US-10-225-567A-229
6	2008	88.0	593	5	US-10-723-860-1006
7	2008	88.0	593	5	US-10-505-486-13
8	2008	88.0	593	6	US-11-199-821-10
9	2002	87.7	593	3	US-09-826-509-563
10	2002	87.7	593	4	US-10-267-730-21
11	2002	87.7	593	5	US-10-925-095-563
12	1957	85.7	595	3	US-09-943-446-6
13	1710	74.9	585	4	US-10-267-730-19
14	1698	74.4	964	4	US-10-017-161-710
15	1698	74.4	964	4	US-10-292-798-622
16	1551	67.9	515	4	US-10-267-730-18
17	1465	64.2	536	4	US-10-372-095-2
18	1130	49.5	542	4	US-10-372-095-4
19	1068	46.8	575	4	US-10-372-095-5
20	1050.5	46.0	550	4	US-10-225-567A-227
21	1050.5	46.0	550	4	US-10-295-027-526
22	1050.5	46.0	550	4	US-10-295-027-851
23	1050.5	46.0	550	5	US-10-723-860-2139
24	1050.5	46.0	561	4	US-10-295-027-524
25	1044.5	45.8	550	3	US-09-826-509-565
26	1044.5	45.8	550	5	US-10-925-095-565
27	1036	45.4	541	3	US-09-996-569-2
28	1036	45.4	541	5	US-10-921-218-2
29	1028.5	45.1	550	4	US-10-014-162-110
30	1011.5	44.3	546	4	US-10-014-162-109
31	776	34.0	459	4	US-10-831-393-4
32	775.5	34.0	1324	3	US-09-935-371-56
33	773.5	33.9	444	4	US-10-831-393-6
34	772	33.8	459	4	US-10-831-393-3
35	772	33.8	459	4	US-10-831-393-8
36	762.5	33.4	458	4	US-10-831-393-5
37	762.5	33.4	458	4	US-10-831-393-7
38	757.5	33.2	449	4	US-10-051-874-68
39	752.5	33.0	457	4	US-10-225-567A-469
40	752.5	33.0	457	4	US-10-292-798-618
41	752.5	33.0	457	4	US-10-831-393-1
42	752.5	33.0	457	6	US-11-199-821-13
43	747	32.7	440	4	US-10-292-798-608
44	747	32.7	440	4	US-10-051-874-64
45	747	32.7	440	4	US-10-051-874-65

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OM protein - protein search, using sw model

Run on: July 26, 2006, 21:40:02 ; Search time 21.5448 Seconds  
 (without alignments)  
 1333.463 Million cell updates/sec

Title: US-09-869-565-2  
 Perfect score: 2283  
 Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGSARPPPLLQEGWETVM 435

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 232337 seqs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	476	20.8	461	6	US-10-505-928-282	Sequence 282, App
2	457.5	20.0	375	7	US-11-358-841-10	Sequence 10, Appl
3	457.5	20.0	415	7	US-11-358-841-9	Sequence 9, Appli
4	455	19.9	309	7	US-11-358-841-13	Sequence 13, Appl
5	453.5	19.9	375	7	US-11-358-841-3	Sequence 3, Appli
6	453.5	19.9	415	7	US-11-358-841-1	Sequence 1, Appli
7	429	18.8	444	7	US-11-358-841-2	Sequence 2, Appli
8	382.5	16.8	401	7	US-11-358-841-4	Sequence 4, Appli
9	381.5	16.7	240	7	US-11-358-841-14	Sequence 14, Appl
10	313.5	13.7	284	6	US-10-504-973-16	Sequence 16, Appl
11	296.5	13.0	341	7	US-11-358-841-7	Sequence 7, Appli
12	287.5	12.6	319	7	US-11-358-841-12	Sequence 12, Appl
13	285.5	12.5	356	7	US-11-358-841-36	Sequence 36, Appl
14	283.5	12.4	370	7	US-11-358-841-6	Sequence 6, Appli
15	281.5	12.3	320	7	US-11-358-841-32	Sequence 32, Appl
16	219	9.6	327	7	US-11-358-841-37	Sequence 37, Appl
17	219	9.6	339	7	US-11-358-841-35	Sequence 35, Appl
18	213	9.3	283	6	US-10-504-973-13	Sequence 13, Appl
19	200.5	8.8	742	7	US-11-289-102-241	Sequence 241, App
20	200.5	8.8	786	6	US-10-504-973-31	Sequence 31, Appl
21	190.5	8.3	1403	6	US-10-505-928-471	Sequence 471, App
22	187	8.2	400	6	US-10-504-973-17	Sequence 17, Appl
23	176	7.7	528	6	US-10-196-749-490	Sequence 490, App
24	175.5	7.7	801	6	US-10-504-973-38	Sequence 38, Appl
25	166	7.3	695	7	US-11-293-697-3126	Sequence 3126, Ap
26	163.5	7.2	687	7	US-11-218-716-8	Sequence 8, Appli
27	156.5	6.9	693	6	US-10-505-928-678	Sequence 678, App
28	156.5	6.9	693	7	US-11-218-716-2	Sequence 2, Appli
29	156.5	6.9	693	7	US-11-218-716-4	Sequence 4, Appli
30	156.5	6.9	693	7	US-11-218-716-6	Sequence 6, Appli
31	149.5	6.5	504	6	US-10-539-228-334	Sequence 334, App
32	149.5	6.5	504	6	US-10-539-228-336	Sequence 336, App
33	144.5	6.3	510	6	US-10-539-228-338	Sequence 338, App
34	144.5	6.3	510	6	US-10-539-228-340	Sequence 340, App
35	134.5	5.9	687	7	US-11-341-947-2	Sequence 2, Appli
36	134.5	5.9	687	7	US-11-218-716-10	Sequence 10, Appl
37	119.5	5.2	686	6	US-10-539-228-331	Sequence 331, App
38	101.5	4.4	352	6	US-10-505-928-745	Sequence 745, App
39	101.5	4.4	352	6	US-10-511-937-2486	Sequence 2486, Ap
40	101.5	4.4	352	6	US-10-511-937-2935	Sequence 2935, Ap
41	101.5	4.4	352	6	US-10-511-937-3010	Sequence 3010, Ap
42	97.5	4.3	335	7	US-11-056-355B-57140	Sequence 57140, A
43	97.5	4.3	407	7	US-11-056-355B-57139	Sequence 57139, A
44	96.5	4.2	197	7	US-11-056-355B-35249	Sequence 35249, A

45 95.5 4.2 362 7 US-11-175-714-130 Sequence 130, App

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8/22/06

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OM protein - protein search, using sw model

Run on: July 26, 2006, 21:23:07 ; Search time 35.5531 Seconds  
(without alignments)  
1016.794 Million cell updates/sec

Title: US-09-869-565-2\_COPY\_23\_435  
Perfect score: 2175  
Sequence: 1 YALEVFDRGLMIYTVGYSMS.....EASGSARPPPLLQEGWETVM 413

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2160	99.3	591	1 US-08-468-249A-20	Sequence 20, Appl
2	1981	91.1	593	2 US-09-631-603-21	Sequence 21, Appl
3	1975	90.8	593	1 US-08-468-249A-21	Sequence 21, Appl
4	1975	90.8	593	2 US-09-826-509-563	Sequence 563, App
5	1702.5	78.3	585	1 US-08-142-439A-6	Sequence 6, Appli
6	1702.5	78.3	585	1 US-08-142-551B-125	Sequence 125, App
7	1702.5	78.3	585	1 US-08-869-477-6	Sequence 6, Appli
8	1702.5	78.3	585	1 US-08-468-249A-19	Sequence 19, Appl
9	1543.5	71.0	515	1 US-08-468-249A-18	Sequence 18, Appl
10	1465	67.4	536	2 US-09-449-632-2	Sequence 2, Appli
11	1130	52.0	542	2 US-09-449-632-4	Sequence 4, Appli
12	1068	49.1	575	2 US-09-449-632-5	Sequence 5, Appli
13	1050.5	48.3	550	2 US-09-631-603-20	Sequence 20, Appl
14	1044.5	48.0	550	2 US-09-826-509-565	Sequence 565, App
15	1036	47.6	541	2 US-08-468-011A-2	Sequence 2, Appli
16	1036	47.6	541	2 US-09-236-468A-2	Sequence 2, Appli
17	1036	47.6	541	5 PCT-US95-07085-2	Sequence 2, Appli
18	960.5	44.2	207	2 US-08-811-519-31	Sequence 31, Appl
19	776	35.7	459	2 US-09-694-519-4	Sequence 4, Appli
20	775.5	35.7	1324	1 US-08-811-897A-56	Sequence 56, Appl
21	775.5	35.7	1324	2 US-09-201-474-56	Sequence 56, Appl
22	773.5	35.6	444	2 US-09-694-519-6	Sequence 6, Appli
23	772	35.5	459	2 US-09-694-519-3	Sequence 3, Appli
24	772	35.5	459	2 US-09-694-519-8	Sequence 8, Appli
25	762.5	35.1	458	1 US-08-112-817C-2	Sequence 2, Appli
26	762.5	35.1	458	2 US-09-694-519-5	Sequence 5, Appli
27	762.5	35.1	458	2 US-09-694-519-7	Sequence 7, Appli
28	755.5	34.7	449	1 US-08-142-439A-5	Sequence 5, Appli
29	755.5	34.7	449	1 US-08-869-477-5	Sequence 5, Appli
30	752.5	34.6	457	2 US-09-631-603-23	Sequence 23, Appl
31	752.5	34.6	457	2 US-09-694-519-1	Sequence 1, Appli
32	747	34.3	440	2 US-09-631-603-22	Sequence 22, Appl
33	746.5	34.3	457	2 US-09-826-509-579	Sequence 579, App
34	741	34.1	460	2 US-09-694-519-2	Sequence 2, Appli
35	738	33.9	440	2 US-09-826-509-567	Sequence 567, App
36	718	33.0	447	2 US-09-694-519-9	Sequence 9, Appli
37	687	31.6	448	1 US-08-811-897A-22	Sequence 22, Appl
38	687	31.6	448	1 US-08-855-213-22	Sequence 22, Appl
39	687	31.6	448	2 US-09-201-474-22	Sequence 22, Appl
40	687	31.6	468	2 US-09-631-603-19	Sequence 19, Appl
41	687	31.6	525	1 US-08-811-897A-23	Sequence 23, Appl
42	687	31.6	525	1 US-08-855-213-23	Sequence 23, Appl
43	687	31.6	525	2 US-09-201-474-23	Sequence 23, Appl
44	684	31.4	448	1 US-08-811-897A-18	Sequence 18, Appl
45	684	31.4	448	1 US-08-855-213-18	Sequence 18, Appl

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OM protein - protein search, using sw model

Run on: July 26, 2006, 21:39:27 ; Search time 126.14 Seconds  
(without alignments)  
1516.626 Million cell updates/sec

Title: US-09-869-565-2\_COPY\_23\_435  
Perfect score: 2175  
Sequence: 1 YALEVFDRLGMIYTVGYSMS.....EASGSARPPPLLQEGWETVM 413

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2160	99.3	591	4	US-10-267-730-20	Sequence 20, Appl
2	2152	98.9	591	3	US-09-943-446-7	Sequence 7, Appli
3	2115	97.2	591	3	US-09-943-446-8	Sequence 8, Appli
4	1981	91.1	593	3	US-09-943-446-9	Sequence 9, Appli
5	1981	91.1	593	4	US-10-225-567A-229	Sequence 229, App
6	1981	91.1	593	5	US-10-723-860-1006	Sequence 1006, Ap
7	1981	91.1	593	5	US-10-505-486-13	Sequence 13, Appl
8	1981	91.1	593	6	US-11-199-821-10	Sequence 10, Appl
9	1975	90.8	593	3	US-09-826-509-563	Sequence 563, App
10	1975	90.8	593	4	US-10-267-730-21	Sequence 21, Appl
11	1975	90.8	593	5	US-10-925-095-563	Sequence 563, App
12	1930	88.7	595	3	US-09-943-446-6	Sequence 6, Appli
13	1702.5	78.3	585	4	US-10-267-730-19	Sequence 19, Appl
14	1698	78.1	964	4	US-10-017-161-710	Sequence 710, App
15	1698	78.1	964	4	US-10-292-798-622	Sequence 622, App
16	1543.5	71.0	515	4	US-10-267-730-18	Sequence 18, Appl
17	1465	67.4	536	4	US-10-372-095-2	Sequence 2, Appli
18	1130	52.0	542	4	US-10-372-095-4	Sequence 4, Appli
19	1068	49.1	575	4	US-10-372-095-5	Sequence 5, Appli
20	1050.5	48.3	550	4	US-10-225-567A-227	Sequence 227, App
21	1050.5	48.3	550	4	US-10-295-027-526	Sequence 526, App
22	1050.5	48.3	550	4	US-10-295-027-851	Sequence 851, App
23	1050.5	48.3	550	5	US-10-723-860-2139	Sequence 2139, Ap
24	1050.5	48.3	561	4	US-10-295-027-524	Sequence 524, App
25	1044.5	48.0	550	3	US-09-826-509-565	Sequence 565, App
26	1044.5	48.0	550	5	US-10-925-095-565	Sequence 565, App
27	1036	47.6	541	3	US-09-996-569-2	Sequence 2, Appli
28	1036	47.6	541	5	US-10-921-218-2	Sequence 2, Appli
29	1028.5	47.3	550	4	US-10-014-162-110	Sequence 110, App
30	1011.5	46.5	546	4	US-10-014-162-109	Sequence 109, App
31	776	35.7	459	4	US-10-831-393-4	Sequence 4, Appli
32	775.5	35.7	1324	3	US-09-935-371-56	Sequence 56, Appl
33	773.5	35.6	444	4	US-10-831-393-6	Sequence 6, Appli
34	772	35.5	459	4	US-10-831-393-3	Sequence 3, Appli
35	772	35.5	459	4	US-10-831-393-8	Sequence 8, Appli
36	762.5	35.1	458	4	US-10-831-393-5	Sequence 5, Appli
37	762.5	35.1	458	4	US-10-831-393-7	Sequence 7, Appli
38	755.5	34.7	449	4	US-10-051-874-68	Sequence 68, Appl
39	752.5	34.6	457	4	US-10-225-567A-469	Sequence 469, App
40	752.5	34.6	457	4	US-10-292-798-618	Sequence 618, App
41	752.5	34.6	457	4	US-10-831-393-1	Sequence 1, Appli
42	752.5	34.6	457	6	US-11-199-821-13	Sequence 13, Appl
43	747	34.3	440	4	US-10-292-798-608	Sequence 608, App
44	747	34.3	440	4	US-10-051-874-64	Sequence 64, Appl
45	747	34.3	440	4	US-10-051-874-65	Sequence 65, Appl

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OM protein - protein search, using sw model

Run on: July 26, 2006, 21:40:02 ; Search time 20.4552 Seconds  
 (without alignments)  
 1333.463 Million cell updates/sec

Title: US-09-869-565-2\_COPY\_23\_435  
 Perfect score: 2175  
 Sequence: 1 YALEVFDRGLMIYTVGYSMS.....EASGSARPPPLQEGWETVM 413

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 232337 seqs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	476	21.9	461	6	US-10-505-928-282 Sequence 282, App
2	455	20.9	309	7	US-11-358-841-13 Sequence 13, Appl
3	455	20.9	375	7	US-11-358-841-10 Sequence 10, Appl
4	455	20.9	415	7	US-11-358-841-9 Sequence 9, Appli
5	452	20.8	375	7	US-11-358-841-3 Sequence 3, Appli
6	452	20.8	415	7	US-11-358-841-1 Sequence 1, Appli
7	427.5	19.7	444	7	US-11-358-841-2 Sequence 2, Appli
8	381.5	17.5	240	7	US-11-358-841-14 Sequence 14, Appl
9	381	17.5	401	7	US-11-358-841-4 Sequence 4, Appli
10	313.5	14.4	284	6	US-10-504-973-16 Sequence 16, Appl
11	295	13.6	341	7	US-11-358-841-7 Sequence 7, Appli
12	285	13.1	319	7	US-11-358-841-12 Sequence 12, Appl
13	283	13.0	356	7	US-11-358-841-36 Sequence 36, Appl
14	282	13.0	370	7	US-11-358-841-6 Sequence 6, Appli
15	279	12.8	320	7	US-11-358-841-32 Sequence 32, Appl
16	216.5	10.0	327	7	US-11-358-841-37 Sequence 37, Appl
17	216.5	10.0	339	7	US-11-358-841-35 Sequence 35, Appl
18	213	9.8	283	6	US-10-504-973-13 Sequence 13, Appl
19	196.5	9.0	742	7	US-11-289-102-241 Sequence 241, App
20	196.5	9.0	786	6	US-10-504-973-31 Sequence 31, Appl
21	190.5	8.8	1403	6	US-10-505-928-471 Sequence 471, App
22	179	8.2	400	6	US-10-504-973-17 Sequence 17, Appl
23	172.5	7.9	528	6	US-10-196-749-490 Sequence 490, App
24	171.5	7.9	801	6	US-10-504-973-38 Sequence 38, Appl
25	166	7.6	695	7	US-11-293-697-3126 Sequence 3126, Ap
26	163.5	7.5	687	7	US-11-218-716-8 Sequence 8, Appli
27	156.5	7.2	693	6	US-10-505-928-678 Sequence 678, App
28	156.5	7.2	693	7	US-11-218-716-2 Sequence 2, Appli
29	156.5	7.2	693	7	US-11-218-716-4 Sequence 4, Appli
30	156.5	7.2	693	7	US-11-218-716-6 Sequence 6, Appli
31	149.5	6.9	504	6	US-10-539-228-334 Sequence 334, App
32	149.5	6.9	504	6	US-10-539-228-336 Sequence 336, App
33	144.5	6.6	510	6	US-10-539-228-338 Sequence 338, App
34	144.5	6.6	510	6	US-10-539-228-340 Sequence 340, App
35	134.5	6.2	687	7	US-11-341-947-2 Sequence 2, Appli
36	134.5	6.2	687	7	US-11-218-716-10 Sequence 10, Appl
37	119.5	5.5	686	6	US-10-539-228-331 Sequence 331, App
38	101.5	4.7	352	6	US-10-505-928-745 Sequence 745, App
39	101.5	4.7	352	6	US-10-511-937-2486 Sequence 2486, Ap
40	101.5	4.7	352	6	US-10-511-937-2935 Sequence 2935, Ap
41	101.5	4.7	352	6	US-10-511-937-3010 Sequence 3010, Ap
42	96.5	4.4	197	7	US-11-056-355B-35249 Sequence 35249, A
43	95.5	4.4	362	7	US-11-175-714-130 Sequence 130, App
44	94.5	4.3	525	6	US-10-449-902-43532 Sequence 43532, A



45 93 4.3 335 7 US-11-056-355B-57140 Sequence 57140, A